

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Withdrawn): A panel of single nucleotide polymorphisms for analyzing compromised nucleic acid samples, comprising two or more single nucleotide polymorphisms, wherein each of the two or more single nucleotide polymorphisms of the panel are selected from single nucleotide polymorphisms that are not genetically linked with respect to one another, and wherein each of the two or more single nucleotide polymorphisms of the panel are selected from single nucleotide polymorphisms that are located outside tandem repeat nucleic acid sequences.
2. (Withdrawn and currently amended): A panel according to claim 1, wherein the single nucleotide polymorphisms include the nucleic acid sequences selected from the group consisting of SEQ ID NOS. 25-36, 61-72, ~~98-109~~ 97-108, ~~134-145~~ 133-144, ~~170-181~~ 169-180, ~~206-217~~ 205-216, ~~242-253~~ 241-252, ~~278-289~~ 277-288, ~~314-325~~ 313-324, ~~351-362~~ 349-360, ~~387-398~~ 385-396, ~~423-434~~ 421-432, and ~~457-467~~ 455-465.
3. (Withdrawn): A method of generating a panel of single nucleotide polymorphisms from a population of interest for analyzing a compromised nucleic acid sample, comprising: selecting a panel of two or more single nucleotide polymorphisms in a genome of the population of interest, wherein each of the two or more single nucleotide polymorphisms of the panel are single nucleotide polymorphisms of the genome that are not genetically linked with respect to one another, and wherein each of the two or more single nucleotide polymorphisms of the panel are single nucleotide polymorphisms of the genome that are located outside tandem repeat nucleic acid sequences, thereby generating the panel of single nucleotide polymorphisms from the population of interest for analyzing the compromised nucleic acid sample.
4. (Withdrawn): A method according to claim 3, wherein the compromised sample comprises nucleic acids from about 10 nucleotides in length to about 100 nucleotides in length.

5. (Withdrawn): A method according to claim 3, wherein the population of interest is human.
6. (Withdrawn): A method according to claim 3, wherein the population of interest is one missing human.
7. (Withdrawn): A method for determining the identity of an individual from an unknown sample of compromised nucleic acids, comprising:
- obtaining the unknown sample of compromised nucleic acids having two or more single nucleotide polymorphisms from an individual;
 - identifying two or more single nucleotide polymorphisms present in the unknown sample of compromised nucleic acids;
 - comparing the identity of each of the two or more single nucleotides polymorphisms in the compromised sample with a panel of single nucleotide polymorphisms from a known sample to determine a number of matches between each of the two or more single nucleotide polymorphisms in the unknown sample and the panel, wherein the panel comprises two or more single nucleotide polymorphisms that are not genetically linked with respect to one another, and are located outside tandem repeat nucleic acid sequences; and
 - determining the probability that the unknown sample and the known sample are derived from the same or related individual based on the number of matches between each of the two or more single nucleotide polymorphism in the unknown sample and the known sample, thereby determining the identity of the individual from the unknown sample of compromised nucleic acids.
8. (Withdrawn): A method for determining the identity of an individual from an unknown sample of compromised nucleic acids, comprising:
- obtaining the unknown sample of compromised nucleic acids having two or more single nucleotide polymorphisms from an individual;
 - obtaining a known sample of nucleic acids having two or more single nucleotide polymorphisms;
 - selecting a panel of two or more single nucleotide polymorphisms, wherein each of the two or more single nucleotide polymorphisms of the panel are not genetically linked with

respect to one another, and wherein each of the single nucleotide polymorphisms of the panel are located outside tandem repeat nucleic acid sequences;

determining the identity of each of the two or more single nucleotide polymorphisms of the panel that are present in the compromised nucleic acid sample; and

determining the identity of each of the two or more single nucleotide polymorphisms of the panel that are present in the known sample;

comparing the identities of the two or more single nucleotide polymorphisms of the panel observed in the known sample with the identities of the two or more single nucleotide polymorphisms of the panel observed in the unknown sample of compromised nucleic acids; and

determining the probability that the unknown sample and the known sample are derived from the same or related individual, thereby determining the identity of the individual from the unknown sample of compromised nucleic acids.

9. (Withdrawn): A method according to claim 7, wherein the known sample and the unknown sample are from the same individual.

10. (Withdrawn): A method according to claim 7, wherein the known sample is from a family member.

11. (Withdrawn): A method according to claim 7, wherein the compromised nucleic acid sample comprises nucleic acid fragments from about 10 nucleotides in length to about 100 nucleotides in length.

12. (Withdrawn): A method according to claim 7, wherein the identity of the one or more single nucleotide polymorphisms is determined using a single base primer extension reaction.

13. (Withdrawn): A method according to claim 7, wherein the two or more of the single nucleotide polymorphisms of the compromised sample are identified in a multiplexed reaction.

14. (Withdrawn): A method according to claim 7, wherein the two or more of the single nucleotide polymorphisms of the panel are identified in a multiplexed reaction.

15. (Withdrawn): A method according to claim 7, wherein the two or more single nucleotide polymorphisms of the panel are identified on an array.

16. (Withdrawn): A method according to claim 7, wherein the two or more single nucleotide polymorphisms of the compromised sample are identified on an array.

17. (Withdrawn): A method according to claim 15, wherein the array is an addressable array.

18. (Withdrawn): A method according to claim 16, wherein the array is an addressable array.

19. (Withdrawn): A method according to claim 15, wherein the array is a virtual array.

20. (Withdrawn): A method according to claim 16, wherein the array is a virtual array.

21. (Previously presented): A method for genotyping a compromised nucleic acid sample, comprising
obtaining the sample of compromised nucleic acids from an individual;
identifying two or more single nucleotide polymorphisms present in the compromised nucleic acid sample; and
comparing the identity of each of the two or more single nucleotides polymorphisms in the compromised sample with a panel of single nucleotide polymorphisms from a population of interest to determine the frequency of occurrence of each of the two or more single nucleotide polymorphism in the compromised sample with the population of interest, wherein the panel comprises two or more single nucleotide polymorphisms that are not genetically linked with respect to one another, and are located outside tandem repeat nucleic acid sequences; thereby genotyping the sample of compromised nucleic acids.

22. (Previously presented): A method for genotyping a compromised nucleic acid sample, comprising
obtaining the sample of compromised nucleic acids from an individual;
selecting a panel of single nucleotide polymorphisms from a genome of a population of interest, the panel comprising two or more single nucleotide polymorphisms, wherein each of the two or more single nucleotide polymorphisms of the panel are single nucleotide polymorphisms that are not genetically linked with respect to one another and are located outside tandem repeat nucleic acid sequences;
identifying two or more single nucleotide polymorphisms present in the compromised nucleic acid sample; and
comparing the identities of the two or more single nucleotide polymorphisms observed in the compromised sample with the identities of the two or more single nucleotide polymorphisms observed in the panel to determine a genotype, thereby obtaining the genotype for the compromised nucleic acid sample.
23. (Previously presented): A genotyping method according to claim 22, wherein the single nucleotide polymorphisms are biallelic and the identities of the alleles of the single nucleotide polymorphisms are T and/or C.
24. (Previously presented): A genotyping method according to claim 22, wherein the population of interest is human.
25. (Previously presented): A genotyping method according to claim 22, wherein the sample comprises human nucleic acids.
26. (Previously presented): A genotyping method according to claim 22, wherein the two or more single nucleotide polymorphisms present in the compromised nucleic acid sample are identified using a single base primer extension reaction.

27. (Previously presented): A genotyping method according to claim 22, wherein the two or more single nucleotide polymorphisms present in the compromised nucleic acid sample are identified in a multiplexed reaction.

28. (Previously presented): A genotyping method according to claim 22, wherein the two or more single nucleotide polymorphisms present in the compromised nucleic acid sample are identified on an array.

29. (Previously presented): A genotyping method according to claim 28, wherein the array is an addressable array.

30. (Previously presented): A genotyping method according to claim 28, wherein the array is a virtual array.

31. (Previously presented): A genotyping method according to claim 22, wherein the compromised nucleic acid sample is amplified to a length of from about 10 nucleotides to about 100 nucleotides.

32. (Previously presented): A genotyping method according to claim 21, wherein 12 to 40 single nucleotide polymorphisms are identified and compared to obtain the genotype for the compromised nucleic acid sample.

33. (Previously presented): A genotyping method according to claim 22, wherein 12 to 40 single nucleotide polymorphisms are identified and compared to obtain the genotype for the compromised nucleic acid sample.

34. (Previously presented): A genotyping method according to claim 21, wherein only single nucleotide polymorphisms that are not genetically linked with respect to one another and are located outside tandem repeat nucleic acid sequences are identified and compared to obtain the genotype for the compromised nucleic acid sample.

35. (Previously presented): A genotyping method according to claim 22, wherein only single nucleotide polymorphisms that are not genetically linked with respect to one another and are located outside tandem repeat nucleic acid sequences are identified and compared to obtain the genotype for the compromised nucleic acid sample.

36. (Currently amended): A genotyping method according to claim 21, wherein the single nucleotide polymorphisms include the nucleic acid sequences selected from the group consisting of SEQ ID NOS. 25-36, 61-72, ~~98-109~~ 97-108, ~~134-145~~ 133-144, ~~170-181~~ 169-180, ~~206-217~~ 205-216, ~~242-253~~ 241-252, ~~278-289~~ 277-288, ~~314-325~~ 313-324, ~~351-362~~ 349-360, ~~387-398~~ 385-396, ~~423-434~~ 421-432, and ~~457-467~~ 455-465.

37. (Currently amended): A genotyping method according to claim 22, wherein the single nucleotide polymorphisms include the nucleic acid sequences selected from the group consisting of SEQ ID NOS. 25-36, 61-72, ~~98-109~~ 97-108, ~~134-145~~ 133-144, ~~170-181~~ 169-180, ~~206-217~~ 205-216, ~~242-253~~ 241-252, ~~278-289~~ 277-288, ~~314-325~~ 313-324, ~~351-362~~ 349-360, ~~387-398~~ 385-396, ~~423-434~~ 421-432, and ~~457-467~~ 455-465.